

## **RAW SEQUENCE LISTING**

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Application Serial Number: 10/502,051  
Source: PCT  
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PATENT APPLICATION: US/10/502,051

DATE: 04/28/2006

TIME: 09:34:20

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 Output Set: N:\CRF4\04282006\J502051.raw

3 <110> APPLICANT: KADOWAKI, TAKASHI  
 4 YAMAUCHI, TOSHIMASA  
 5 KAMON, JUNJI  
 6 WAKI, HIRONORI  
 7 NAGAI, RYOZO  
 8 KIMURA, SATOSHI  
 9 TOMITA, MOTOO  
 11 <120> TITLE OF INVENTION: INSULIN RESISTANCE IMPROVING AGENT  
 13 <130> FILE REFERENCE: 256653US0PCT  
 15 <140> CURRENT APPLICATION NUMBER: 10/502,051  
 16 <141> CURRENT FILING DATE: 2004-07-30  
 18 <150> PRIOR APPLICATION NUMBER: PCT/JP02/07599  
 19 <151> PRIOR FILING DATE: 2002-07-26  
 21 <150> PRIOR APPLICATION NUMBER: JP 2002-23554  
 22 <151> PRIOR FILING DATE: 2002-01-31  
 24 <160> NUMBER OF SEQ ID NOS: 4  
 26 <170> SOFTWARE: PatentIn version 3.3  
 28 <210> SEQ ID NO: 1  
 29 <211> LENGTH: 735  
 30 <212> TYPE: DNA  
 31 <213> ORGANISM: Homo sapiens  
 34 <220> FEATURE:  
 35 <221> NAME/KEY: CDS  
 36 <222> LOCATION: (1)..(735)  
 38 <400> SEQUENCE: 1  
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 41 1 5 10 15  
 43 gac cag gaa acc acg act caa ggg ccc gga gtc ctg ctt ccc ctg ccc 96  
 44 Asp Gln Glu Thr Thr Gln Gly Pro Gly Val Leu Leu Pro Leu Pro  
 45 20 25 30  
 47 aag ggg gcc tgc aca ggt tgg atg gcg ggc atc cca ggg cat ccg ggc 144  
 48 Lys Gly Ala Cys Thr Gly Trp Met Ala Gly Ile Pro Gly His Pro Gly  
 49 35 40 45  
 51 cat aat ggg gcc cca ggc cgt gat ggc aga gat ggc acc cct ggt gag 192  
 52 His Asn Gly Ala Pro Gly Arg Asp Gly Arg Asp Gly Thr Pro Gly Glu  
 53 50 55 60  
 55 aag ggt gag aaa gga gat cca ggt ctt att ggt cct aag gga gac atc 240  
 56 Lys Gly Glu Lys Gly Asp Pro Gly Leu Ile Gly Pro Lys Gly Asp Ile  
 57 65 70 75 80  
 59 ggt gaa acc gga gta ccc ggg gct gaa ggt ccc cga ggc ttt ccg gga 288  
 60 Gly Glu Thr Gly Val Pro Gly Ala Glu Gly Pro Arg Gly Phe Pro Gly  
 61 85 90 95

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63 atc caa ggc agg aaa gga gaa cct gga gaa ggt gcc tat gta tac cgc	336
64 Ile Gln Gly Arg Lys Gly Glu Pro Gly Glu Gly Ala Tyr Val Tyr Arg	
65 100 105 110	
67 tca gca ttc agt gtg gga ttg gag act tac gtt act atc ccc aac atg	384
68 Ser Ala Phe Ser Val Gly Leu Glu Thr Tyr Val Thr Ile Pro Asn Met	
69 115 120 125	
71 ccc att cgc ttt acc aag atc ttc tac aat cag caa aac cac tat gat	432
72 Pro Ile Arg Phe Thr Lys Ile Phe Tyr Asn Gln Gln Asn His Tyr Asp	
73 130 135 140	
75 ggc tcc act ggt aaa ttc cac tgc aac att cct ggg ctg tac tac ttt	480
76 Gly Ser Thr Gly Lys Phe His Cys Asn Ile Pro Gly Leu Tyr Tyr Phe	
77 145 150 155 160	
79 gcc tac cac atc aca gtc tat atg aag gat gtg aag gtc agc ctc ttc	528
80 Ala Tyr His Ile Thr Val Tyr Met Lys Asp Val Lys Val Ser Leu Phe	
81 165 170 175	
83 aag aag gac aag gct atg ctc ttc acc tat gat cag tac cag gaa aat	576
84 Lys Lys Asp Lys Ala Met Leu Phe Thr Tyr Asp Gln Tyr Gln Glu Asn	
85 180 185 190	
87 aat gtg gac cag gcc tcc ggc tct gtg ctc ctg cat ctg gag gtg ggc	624
88 Asn Val Asp Gln Ala Ser Gly Ser Val Leu Leu His Leu Glu Val Gly	
89 195 200 205	
91 gac caa gtc tgg ctc cag gtg tat ggg gaa gga gag cgt aat gga ctc	672
92 Asp Gln Val Trp Leu Gln Val Tyr Gly Glu Gly Glu Arg Asn Gly Leu	
93 210 215 220	
95 tat gct gat aat gac aat gac tcc acc ttc aca ggc ttt ctt ctc tac	720
96 Tyr Ala Asp Asn Asp Asn Asp Ser Thr Phe Thr Gly Phe Leu Leu Tyr	
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106 <212> TYPE: PRT	
107 <213> ORGANISM: Homo sapiens	
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116 20 25 30	
119 Lys Gly Ala Cys Thr Gly Trp Met Ala Gly Ile Pro Gly His Pro Gly	
120 35 40 45	
123 His Asn Gly Ala Pro Gly Arg Asp Gly Arg Asp Gly Thr Pro Gly Glu	
124 50 55 60	
127 Lys Gly Glu Lys Gly Asp Pro Gly Leu Ile Gly Pro Lys Gly Asp Ile	
128 65 70 75 80	
131 Gly Glu Thr Gly Val Pro Gly Ala Glu Gly Pro Arg Gly Phe Pro Gly	
132 85 90 95	
135 Ile Gln Gly Arg Lys Gly Glu Pro Gly Glu Gly Ala Tyr Val Tyr Arg	
136 100 105 110	
139 Ser Ala Phe Ser Val Gly Leu Glu Thr Tyr Val Thr Ile Pro Asn Met	

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144	130	135	140	
147	Gly Ser Thr Gly Lys Phe His Cys Asn Ile Pro Gly Leu Tyr Tyr Phe			
148	145 150	155	160	
151	Ala Tyr His Ile Thr Val Tyr Met Lys Asp Val Lys Val Ser Leu Phe			
152	165	170	175	
155	Lys Lys Asp Lys Ala Met Leu Phe Thr Tyr Asp Gln Tyr Gln Glu Asn			
156	180	185	190	
159	Asn Val Asp Gln Ala Ser Gly Ser Val Leu Leu His Leu Glu Val Gly			
160	195	200	205	
163	Asp Gln Val Trp Leu Gln Val Tyr Gly Glu Gly Glu Arg Asn Gly Leu			
164	210	215	220	
167	Tyr Ala Asp Asn Asp Asn Asp Ser Thr Phe Thr Gly Phe Leu Leu Tyr			
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171	His Asp Thr Asn			
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176	<211> LENGTH: 1276			
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181	<220> FEATURE:			
182	<221> NAME/KEY: CDS			
183	<222> LOCATION: (46)..(789)			
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187	Met Leu Leu Leu			
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190	caa gct ctc ctg ttc ctc tta atc ctg ccc agt cat gcc gaa gat gac			
191	Gln Ala Leu Leu Phe Leu Leu Ile Leu Pro Ser His Ala Glu Asp Asp			105
192	5 10 15 20			
194	gtt act aca act gaa gag cta gct cct gct ttg gtc cct cca ccc aag	153		
195	Val Thr Thr Glu Glu Leu Ala Pro Ala Leu Val Pro Pro Pro Lys			
196	25 30 35			
198	gga act tgt gca ggt tgg atg gca ggc atc cca gga cat cct ggc cac	201		
199	Gly Thr Cys Ala Gly Trp Met Ala Gly Ile Pro Gly His Pro Gly His			
200	40 45 50			
202	aat ggc aca cca ggc cgt gat ggc aga gat ggc act cct gga gag aag	249		
203	Asn Gly Thr Pro Gly Arg Asp Gly Arg Asp Gly Thr Pro Gly Glu Lys			
204	55 60 65			
206	gga gag aaa gga gat gca ggt ctt ctt ggt cct aag ggt gag aca gga	297		
207	Gly Glu Lys Gly Asp Ala Gly Leu Leu Gly Pro Lys Gly Glu Thr Gly			
208	70 75 80			
210	gat gtt gga atg aca gga gct gaa ggg cca cgg ggc ttc ccc gga acc	345		
211	Asp Val Gly Met Thr Gly Ala Glu Gly Pro Arg Gly Phe Pro Gly Thr			
212	85 90 95 100			
214	cct ggc agg aaa gga gag cct gga gaa gcc gct tat atg tat cgc tca	393		
215	Pro Gly Arg Lys Gly Glu Pro Gly Glu Ala Ala Tyr Met Tyr Arg Ser			
216	105 110 115			
218	gcg ttc agt gtg ggg ctg gag acc cgc gtc act gtt ccc aat gta ccc	441		

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219	Ala	Phe	Ser	Val	Gly	Leu	Glu	Thr	Arg	Val	Thr	Val	Pro	Asn	Val	Pro	
220				120			125					130					
222	att	cgc	ttt	act	aag	atc	ttc	tac	aac	caa	cag	aat	cat	tat	gac	ggc	489
223	Ile	Arg	Phe	Thr	Lys	Ile	Phe	Tyr	Asn	Gln	Gln	Asn	His	Tyr	Asp	Gly	
224					135				140			145					
226	agc	act	ggc	aag	ttc	tac	tgc	aac	att	ccg	gga	ctc	tac	tac	ttc	tct	537
227	Ser	Thr	Gly	Lys	Phe	Tyr	Cys	Asn	Ile	Pro	Gly	Leu	Tyr	Tyr	Phe	Ser	
228					150				155			160					
230	tac	cac	atc	acg	gtg	tac	atg	aaa	gat	gtg	aag	gtg	agc	ctc	ttc	aag	585
231	Tyr	His	Ile	Thr	Val	Tyr	Met	Lys	Asp	Val	Lys	Val	Ser	Leu	Phe	Lys	
232					165			170			175				180		
234	aag	gac	aag	gcc	gtt	ctc	ttc	acc	tac	gac	cag	tat	cag	gaa	aag	aat	633
235	Lys	Asp	Lys	Ala	Val	Leu	Phe	Thr	Tyr	Asp	Gln	Tyr	Gln	Glu	Lys	Asn	
236					185				190			195					
238	gtg	gac	cag	gcc	tct	ggc	tct	gtg	ctc	ctc	cat	ctg	gag	gtg	gga	gac	681
239	Val	Asp	Gln	Ala	Ser	Gly	Ser	Val	Leu	Leu	His	Leu	Glu	Val	Gly	Asp	
240					200				205			210					
242	caa	gtc	tgg	ctc	cag	gtg	tat	ggg	gat	ggg	gac	cac	aat	gga	ctc	tat	729
243	Gln	Val	Trp	Leu	Gln	Val	Tyr	Gly	Asp	Gly	Asp	His	Asn	Gly	Leu	Tyr	
244					215			220			225						
246	gca	gat	aac	gtc	aac	gac	tct	aca	ttt	act	ggc	ttt	ctt	ctc	tac	cat	777
247	Ala	Asp	Asn	Val	Asn	Asp	Ser	Thr	Phe	Thr	Gly	Phe	Leu	Leu	Tyr	His	
248					230			235			240						
250	gat	acc	aac	tga	ctgcaactac	ccatagccca	tacaccagga	gaatcatgga									829
251	Asp	Thr	Asn														
252	245																
254	acagtcgaca	cacttcagc	ttagttttag	agattgattt	tattgcttag	tttgagagtc											889
256	ctgagtatta	tccacacgtg	tactcaactg	ttcattaaac	gactttataa	aaaataattt											949
258	gtgttcctag	tccagaaaaa	aaggcactcc	ctggctcaca	cgactcttac	atgttagcaa											1009
260	taacagaatg	aaaatcacat	ttggtatggg	ggcttcacaa	tattcgcatg	actgtctgga											1069
262	agtagaccat	gctattttc	tgctcaactgt	acacaaatat	tgttcacata	aaccctataa											1129
264	tgtaaatatg	aaatacagtg	attactcttc	tcacaggctg	agtgtatgaa	tgtctaaaga											1189
266	cccatataagta	ttaaaatgtgt	agggataaaat	tgaaaaaaa	aaaaaaaaaa	aagaaaaact											1249
268	ttagagcaca	ctggcgcccg	ttactag														1276
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273	<212>	TYPE:	PRT														
274	<213>	ORGANISM:	Mus	musculus													
276	<400>	SEQUENCE:	4														
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282	Ala	Glu	Asp	Asp	Val	Thr	Thr	Glu	Glu	Leu	Ala	Pro	Ala	Leu	Val		
283					20			25			30						
286	Pro	Pro	Pro	Lys	Gly	Thr	Cys	Ala	Gly	Trp	Met	Ala	Gly	Ile	Pro	Gly	
287				35			40			45							
290	His	Pro	Gly	His	Asn	Gly	Thr	Pro	Gly	Arg	Asp	Gly	Arg	Asp	Gly	Thr	
291				50			55			60							
294	Pro	Gly	Glu	Lys	Gly	Glu	Lys	Gly	Asp	Ala	Gly	Leu	Leu	Gly	Pro	Lys	
295	65			70				75			80						

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298 Gly Glu Thr Gly Asp Val Gly Met Thr Gly Ala Glu Gly Pro Arg Gly  
299 85 90 95  
302 Phe Pro Gly Thr Pro Gly Arg Lys Gly Glu Pro Gly Glu Ala Ala Tyr  
303 100 105 110  
306 Met Tyr Arg Ser Ala Phe Ser Val Gly Leu Glu Thr Arg Val Thr Val  
307 115 120 125  
310 Pro Asn Val Pro Ile Arg Phe Thr Lys Ile Phe Tyr Asn Gln Gln Asn  
311 130 135 140  
314 His Tyr Asp Gly Ser Thr Gly Lys Phe Tyr Cys Asn Ile Pro Gly Leu  
315 145 150 155 160  
318 Tyr Tyr Phe Ser Tyr His Ile Thr Val Tyr Met Lys Asp Val Lys Val  
319 165 170 175  
322 Ser Leu Phe Lys Lys Asp Lys Ala Val Leu Phe Thr Tyr Asp Gln Tyr  
323 180 185 190  
326 Gln Glu Lys Asn Val Asp Gln Ala Ser Gly Ser Val Leu Leu His Leu  
327 195 200 205  
330 Glu Val Gly Asp Gln Val Trp Leu Gln Val Tyr Gly Asp Gly Asp His  
331 210 215 220 240  
334 Asn Gly Leu Tyr Ala Asp Asn Val Asn Asp Ser Thr Phe Thr Gly Phe  
335 225 230 235 240  
338 Leu Leu Tyr His Asp Thr Asn  
339 245

**VERIFICATION SUMMARY**  
PATENT APPLICATION: **US/10/502,051**

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